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BD015361
LOCUS          BD015361             822 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Human protein and cDNA[4].
ACCESSION    BD015361
VERSION      BD015361.1 GI:22556499
KEYWORDS     JP 2001218584-A/7.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 822)
AUTHORS      Kato, S. and Saeki, M.
TITLE        Human protein and cDNA[4]
JOURNAL      JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2001218584-A/7
              PD 14-AUG-2001
              PF 08-FEB-2000 JP 2000031062
              PI SEIJI KATO,MIHORO SAEKI
              PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
              C12N5/10//
              CC C12P21/08,C12N15/00,C12N5/00
              FH Key Location/Qualifiers
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              source
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              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT    210 a 186 c 199 g 227 t
ORIGIN
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Pred. No.:      9,2e-69      Length:      822
Score:          918.00      Matches:      178
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              Gaps:      0

US-10-029-137-2 (1-178) x BD015361 (1-822)

QY      1 MetAlaAlaProLeuGlyGlyMetPheSerGlyGlnProGlyProGlnAlaPro 20
DB      10 ATGGCGGCTCCACTAGGGGGTATGTTTCTGGGAGACACCCGGTCCCGCTCAGGCCCG 69
QY      21 ProGlyLeuProGlyGlnAlaSerLeuGlnAlaAlaProGlyAlaProArgProSer 40
DB      70 CCGGGCCCTTCGGGGCCAAAGCTTCGCTTCTTCAGGCAGCTCCAGGCGCTCCAGACCTTCC 129
QY      41 SerSerThrLeuValAspGluLeuGluSerPheGluAlaCysPheAlaSerLeuVal 60
DB      130 AGCAGTACTTTGGTGGAGAGTTGGAGTCACTCTTCGAGGCTTGGTTCATCTCTGGTG 189
QY      61 SerGlnAspTyrValAsnGlyThrAspGlnGluLulleArgThrGlyValAspGlnCys 80
DB      190 AGTCAGGACTATGTCAATGGCCACCGATCAGGAAGAAATTCGAACCGGTGTGTGATCAGTGT 249
QY      81 IleGlnLysPheLeuAspIleAlaArgGlnThrGluCysPhePheLeuGlnLysArgLeu 100
DB      250 ATCCAGAGTTTCTGGATATTTCNAGACAGACAGAAATGTTTTTCTTACAAAAGATTG 309
QY      101 GlnLeuSerValGlnLysProGluGlnValIleLysGluAspValSerGluLeuArgAsn 120
DB      310 CAGTTATCTGTCCAGAAACCCAGAGCAAGTTATCAAAAGAGGATGTGTCAAGAACTAAGGAAT 369
QY      121 GluLeuGlnArgLysAspAlaLeuValGlnLysHisLeuThrLysLeuArgHisTrpGln 140
DB      370 GAATTACAGCGGAAGATGCATAGTCCAGAAAGCACTTGACAAAGCTGAGGCAATTGGCAG 429
QY      141 GlnValLeuGluAspIleAsnValGlnHisLysLysProAlaAspIleProGlnGlySer 160

430 CAGGTCTCGAGACATCAACGTGCAGCACAACAAACCCGCGCATCCCTCAGGGGTCC 489
161 LeuAlaTyrLeuGluGlnAlaSerAlaAsnIleProAlaProLeuLysProThr 178
490 TTGGCTTACTCGAGCAGGCATCTGCCAACATCCCTGCACCTCTGAAGCCAAAG 543

RESULT 2
AX014817
LOCUS          AX014817             882 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION    Sequence 3 from Patent WO9953040.
ACCESSION    AX014817
VERSION      AX014817.1 GI:10041084
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
              Pilarek,C.
TITLE        Human nucleic acid sequences from ovarian tumour tissue
JOURNAL      Patent: WO 9953040-A 3 21-OCT-1999;
              SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
              BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GRS FUER GENOMPORSCHUN
              (DE); PILARSKY CHRISTIAN (DE)
FEATURES     Location/Qualifiers
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              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT    238 a 190 c 206 g 248 t
ORIGIN
Alignment Scores:
Pred. No.:      9,95e-69      Length:      882
Score:          918.00      Matches:      178
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              Gaps:      0

US-10-029-137-2 (1-178) x AX014817 (1-882)

QY      1 MetAlaAlaProLeuGlyGlyMetPheSerGlyGlnProGlyProGlnAlaPro 20
DB      10 ATGGCGGCTCCACTAGGGGGTATGTTTCTGGGAGACACCCGGTCCCGCTCAGGCCCG 69
QY      21 ProGlyLeuProGlyGlnAlaSerLeuGlnAlaAlaProGlyAlaProArgProSer 40
DB      70 CCGGGCCCTTCGGGGCCAAAGCTTCGCTTCTTCAGGCAGCTCCAGGCGCTCCAGACCTTCC 129
QY      41 SerSerThrLeuValAspGluLeuGluSerPheGluAlaCysPheAlaSerLeuVal 60
DB      130 AGCAGTACTTTGGTGGAGAGTTGGAGTCACTCTTCGAGGCTTGGTTCATCTCTGGTG 189
QY      61 SerGlnAspTyrValAsnGlyThrAspGlnGluLulleArgThrGlyValAspGlnCys 80
DB      190 AGTCAGGACTATGTCAATGGCCACCGATCAGGAAGAAATTCGAACCGGTGTGTGATCAGTGT 249
QY      81 IleGlnLysPheLeuAspIleAlaArgGlnThrGluCysPhePheLeuGlnLysArgLeu 100
DB      250 ATCCAGAGTTTCTGGATATTTCNAGACAGACAGAAATGTTTTTCTTACAAAAGATTG 309
QY      101 GlnLeuSerValGlnLysProGluGlnValIleLysGluAspValSerGluLeuArgAsn 120
DB      310 CAGTTATCTGTCCAGAAACCCAGAGCAAGTTATCAAAAGAGGATGTGTCAAGAACTAAGGAAT 369
QY      121 GluLeuGlnArgLysAspAlaLeuValGlnLysHisLeuThrLysLeuArgHisTrpGln 140
DB      370 GAATTACAGCGGAAGATGCATAGTCCAGAAAGCACTTGACAAAGCTGAGGCAATTGGCAG 429
QY      141 GlnValLeuGluAspIleAsnValGlnHisLysLysProAlaAspIleProGlnGlySer 160

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